

SEQUENCE LISTING



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<20> Production of Antibodies

<130> PNK/060113/0275850 - T7060C

<140> US 09/737,476

<141> 2000-12-18

<150> EP 99310188.0

<151> 1999-12-17

<160> 67

<170> MS Word

<210> 1

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH with peptide linker

<220>

<221> CDS

<222> (1)...(417)

<400> 1

cag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct ggg ggc
 Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

48

tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt ggt cat
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 20 25 30

96

ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag gag cgt
 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 35 40 45

144

gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg tat aaa
 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 50 55 60

192

gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc aag act 240
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
65 70 75 80

acg gtt tat ctg caa atg aac aac ctg aaa cct gaa gat acg gcc gtt 288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336
Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
100 105 110

gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384
Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

gaa caa aaa ctc atc tca gaa gag gat ctg aat taataaggc taagctcgaa 437
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
130 135

ttc 440

<210> 2

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> VH with peptide linker

<400> 2

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
20 25 30

Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
35 40 45

Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
100 105 110

Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
130 135

<210> 3

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> myc linker

<400> 3

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

<210> 4

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(459)

<400> 4

cag gtg cag ctg cag cag tca ggg gga ggc ttg gtg cag gct ggg ggg
Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

48

tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
20 25 30

96

cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

144

gca act att agt cct ggt agt agc aca cac tat gta gac tcc gtg aag
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
50 55 60

192

ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct 288
 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc 336
 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
 100 105 110

ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg 384
 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
 115 120 125

gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc 432
 Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
 130 135 140

tca gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 471
 Ser Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

<210> 5

<211> 153

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 5

Gln Val Gln Leu Gln Gln Ser Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
 20 25 30

His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
 35 40 45

Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
 115 120 125

Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
 130 135 140

Ser Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

<210> 6

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> VH with linker

<220>

<221> CDS

<222> (1)..(456)

<400> 6

cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg
 Gln Val Gln Leu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

48

tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
 20 25 30

96

gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc
 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
 35 40 45

144

gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag
 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

192

ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

240

caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct
 Gln Met Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

288

gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg
 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

336

gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc
 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
 115 120 125

384

gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca 432
Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
130 135 140

gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 468
Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<210> 7

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> VH with linker

<400> 7

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
115 120 125

Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
130 135 140

Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<210> 8

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(450)

<400> 8

acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
20 25 30

agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
35 40 45

gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
50 55 60

gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
65 70 75 80

acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt 288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc 336
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat 384
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
115 120 125

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 432
His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
130 135 140

gat ctg aat ggg gcc gca tagtaacaat tg 462
Asp Leu Asn Gly Ala Ala
145 150

<210> 9

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 9

Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
20 25 30

Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
35 40 45

Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
50 55 60

Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
115 120 125

His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
130 135 140

Asp Leu Asn Gly Ala Ala
145 150

<210> 10

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(459)

<400> 10

acc atg gcc cag gtg aaa ctg cag cag tct	ggg gga gga ttg	gtg cag	48
Thr Met Ala Gln Val Lys Leu Gln Gln Ser	Gly Gly Gly	Leu Val Gln	
1 5 10 15			
gct ggg ggc cct ctg agg ctc tcc tgc tgc	gcc tct gga cgc acc ttc		96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser	Gly Arg Thr Phe		
20 25 30			
agt aac tat gcc gtg ggc tgg ttc cgc cag	gct cca ggg aag gag cgt		144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro	Gly Lys Glu Arg		
35 40 45			
gag ttt gtc gct gct att agc cgt gat ggt	ggg cgc aca tac tat gcg		192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly	Gly Arg Thr Tyr Tyr Ala		
50 55 60			
gac tcc gtg aag ggc cga ttc gcc gtc tcc	aga gac tac gcc gag aac		240
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp	Tyr Ala Glu Asn		
65 70 75 80			
acg gtg tat ctg caa atg aac agc ctg aac	cct gag gac acg gcc gtt		288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro	Glu Asp Thr Ala Val		
85 90 95			
tat tac tgt aac aca agg gcc tac tgg ggc	cag ggg acc cag gtc acc		336
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln	Gly Thr Gln Val Thr		
100 105 110			
gtc tcc tca gcg cac cac agc gaa gac ccc	agc tcc gcg gcc cat		384
Val Ser Ser Ala His His Ser Glu Asp Pro Ser	Ser Ala Ala His		
115 120 125			
cac cat cac cat cac ggg gcc gca gaa caa	aaa ctc atc tca gaa gag		432
His His His His Gly Ala Ala Glu Gln Lys Leu	Ile Ser Glu Glu		
130 135 140			
gat ctg aat agt gag aaa gat gag cta tgataacaat	tg		471
Asp Leu Asn Ser Glu Lys Asp Glu Leu			
145 150			

<210> 11

<211> 153

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 11

Thr Met Ala Gln Val Lys Leu Gln Gln Ser	Gly Gly Gly	Leu Val Gln	
1 5 10 15			

Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser	Gly Arg Thr Phe		
20 25 30			

Ser Asn Tyr 'Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg			
35	40	45	
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala			
50	55	60	
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn			
65	70	75	80
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val			
85	90	95	
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr			
100	105	110	
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His			
115	120	125	
His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu			
130	135	140	

Asp Leu Asn Ser Glu Lys Asp Glu Leu
145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 12

agctgcgatc gcaagcttgg taccggaaat tctctaga

38

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 13

aatttctaga gaattcccg tccaaatgtt gcttgcgatc gc

42

<210> 14

<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 14
tcgacccatg gccccgtacg caattggagc t 31

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 15
ccaaattggct agcggggcat ggg 23

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 16
ccaccccacgaa gggaaacatcg tg 22

<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence
<220>
<223> primer

卷之三

400> 17
gaattcccat ggtttacact cgaggccctc tccaaatga 39

<210> 18
<211> 189
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR product
<400> 18

ccaccacacga gggaaacatcg tggaaaaaga agacgttca accacgttctt caaagcaagt 60
ggattgtatgt gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca 120
agacccttcc tttatataag gaagttcatt tcattttggag aggacctcga gtgttaacca 180
tgggaattc 189

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> sequencing primer
<400> 19

ccggcaacag gattcaatct 21

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 20

aqctccatgg qattttgtct cttttcacaa ttgccttcat 40

<210> 21	
<211> 35	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic insert	
<400> 21	
ttctttcttgt ctctacactt ctcttattcc tagta	35
<210> 22	
<211> 35	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic insert	
<400> 22	
atatcccaact cttgccgtgc ccaggtgcag ctgca	35
<210> 23	
<211> 48	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic insert	
<400> 23	
gctgcacctg ggcacggcaa gagtgggata ttactaggaa taagagaa	48
<210> 24	
<211> 54	
<212> DNA	
<213> Artificial Sequence	

<220>
<223> synthetic insert
<400> 24
gtgtagagac aagaagaaaat gaaggcaatt gtgaaaagag aacaatccc atgg 54

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 25
gaaacagct atgaccatga ttac 24

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 26
ttcccgatc acgacgttgt 20

<210> 27
<211> 107
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic fragment encoding PR1a leader
<220>
<221> CDS
<222> (3)...(104)

<400> 27

cc atg gga ttt gtt ctc ttt tca caa ttg cct tca ttt ctt ctt gtc 47
 Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val
 1 5 10 15

tct aca ctt ctc tta ttc cta gta ata tcc cac tct tgc cgt gcc cag 95
 Ser Thr Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln
 20 25 30

gtg cag ctg cag 107
 Val Gln Leu

<210> 28

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic fragment encoding PR1a leader

<400> 28

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser 55
 1 5 10 15

Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln Val
 20 25 30

Gln Leu

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 29

gacatcccat ggcaaggatc a 21

<210> 30

<211> 21

<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 30
aagcttgtta acagccctta a 21

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 31
agggctgtta acaaacttga t 21

<210> 32
<211> 44
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 32
agactgtgc agctgcacct gcttccaca aacaatggta gctg 44

<210> 33
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> sequencing primer
<400> 33

aatttaaccctt cactaaagg

19

<210> 34
 <211> 254
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> GBSS leader
 <220>
 <221> CDS
 <222> (3)..(254)
 <400> 34

cc atg gca agc atc aca gct tca cac cac ttt gtg tca aga agc caa 47
 Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln
 1 5 10 15

act tca cta gac acc aaa tca acc ttg tca cag ata gga ctc agg aac 95
 Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn
 20 25 30

cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg 143
 His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly
 35 40 45

ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga 191
 Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg
 50 55 60

act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa 239
 Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys
 65 70 75

cag gtg cag ctg cag 254
 Gln Val Gln Leu Gln
 80

<210> 35
 <211> 84
 <212> PRT
 <220>
 <223> GBSS leader
 <213> Artificial Sequence
 <400> 35

Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln Thr
1 5 10 15

Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn His
20 25 30

Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly Leu
35 40 45

Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg Thr
50 55 60

Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys Gln
65 70 75 80

Val Gln Leu Gln

THE END 9/14/76 0
<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 36
catgcaggta cagctgca 18

<210> 37
<211> 10
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic insert
<400> 37
gctgcacactg 10

<210> 38
<211> 24
<212> DNA

***** 34/5/60

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 38

cgcaagaccc ttcctctata taag

24

<210> 39

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 39

gagctcgaaat tcttattata gctcatcttt ctctgaattc agatcctttt ctgagatgag 60

<210> 40

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 40

Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
20 25

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 41

atcctcaact tccaaatcaga	20
<210> 42	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> PCR primer	
<400> 42	
ttcttgagag atagcttga	19
<210> 43	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic insert	
<400> 43	
gatcccatgg cccgctagcc aattggagct	30
<210> 44	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic insert	
<400> 44	
ccaattggct agcggggcat gg	22
<210> 45	
<211> 29	
<212> DNA	

40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 45

gatccacac gaggtaaac catggcccg

29

<210> 46

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic insert

<400> 46

cttagcgggcc atggtttaca ctcgagggtg

29

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 47

attgcctacg gcagccgctg

20

<210> 48

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 48

tccaaaccaat tgttactatg cggccccatt cagatccctt tctgagatga g

51

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> sequencing primer
<400> 49
gtctgtctaa agtaaagtag atgcg 25

<210> 50
<211> 60
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 50
tccaaccaat tgttatcata gctcatcttt ctcaactatcc agatcctctt ctgagatgag 60

<210> 51
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 51
agtccccccat ggtacgtcct gttagaaacc 29

<210> 52
<211> 25
<212> DNA
<213> Artificial Sequence

<220>		
<223> PCR primer		
<400> 52		
cgttttcgtc ggttaatcacc attcc		25
<210> 53		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> sequencing primer		
<400> 53		
cgcaagaccc ttcctttata taag		24
<210> 54		
<211> 1154		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> HCV33-hinge-CH2-CH3		
<220>		
<221> CDS		
<222> (3)..(1136)		
<400> 54		
cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct		47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala		
1 5 10 15		
ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt		95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser		
20 25 30		
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag		143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys		
35 40 45		
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg		191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp		
50 55 60		

EQUATION 60

tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala 65 70 75	239
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr 80 85 90 95	287
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser 100 105 110	335
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val 115 120 125	383
tcc tca gaa ccc aag aca cca aaa cca cca caa cca caa cca caa Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln 130 135 140	431
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala 145 150 155	479
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc Pro Glu Leu Leu Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro 160 165 170 175	527
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val 180 185 190	575
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile 195 200 205	623
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac agc acg tac cgc gtc gtc agc gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
cgg gag ccg cag gtg tac gcc ctg gcc cca cac ccg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911

gat atc aac'gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc	959
Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly	
305 310 315	
acc tac gcc acc acg cca ccc cag ctg gac aac gag gac ggg acc tac ttc	1007
Thr Tyr Ala Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe	
320 325 330 335	
ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag ccg gga gaa	1055
Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu	
340 345 350 355	
acc ttc acc tgc gtg atg cac gag gcc ctg cac aac cac tac acc	1103
Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr	
355 360 365	
cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa	1154
Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys	
370 375	
<210> 55	
<211> 377	
<212> PRT	
<213> Artificial Sequence	
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<223> HCV33-hinge-CH2-CH3	
<400> 55	
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly	
1 5 10 15	
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly	
20 25 30	
His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu	
35 40 45	
Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr	
50 55 60	
Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys	
65 70 75 80	
Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala	
85 90 95	
Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu	
100 105 110	
Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser	
115 120 125	

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Ser Glu Pro 'Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro
 130 135 140
 Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160
 Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175
 Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190
 Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205
 Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240
 Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270
 Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285
 Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300
 Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320
 Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335
 Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350
 Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365
 Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial Sequence

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

<220>

<221> CDS

<222> (3)...(1154)

<400> 56

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct	47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala	
1 5 10 15	
ggg ggc tct ctg aca ctc tcc tgt gca gcc tcg gga cgc gcc acc agt	95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser	
20 25 30	
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag	143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys	
35 40 45	
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg	191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp	
50 55 60	
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc	239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	
65 70 75	
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg	287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr	
80 85 90 95	
gcc gtt tat tat tgt gcc gct cga ccc gtc cgc gtg gat gat att tcc	335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser	
100 105 110	
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc	383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val	
115 120 125	
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca caa	431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln	
130 135 140	
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc	479
Pro Pro Gln Pro Asn Pro Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala	
145 150 155	
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccc aaa ccc	527
Pro Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro	
160 165 170 175	
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg	575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val	
180 185 190	
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att	623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile	
195 200 205	

gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa gag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac acg acg tac cgc gtg gtc acg gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
ccg gag ccg cag gtg tac gcc ctg gcc cca cac ccg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911
gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly 305 310 315	959
acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe 320 325 330 335	1007
ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag ccg gga gaa Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu 340 345 350	1055
acc ttc acc tgt gtg atg cac gag gcc ctg cac aac cac tac acc Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr 355 360 365	1103
cag aaa tcc atc acc cag tct tcg ggt aaa tct gag aaa gat gag cta Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu 370 375 380	1151
taa taagaattc agctcgaa	1172
<210> 57	
<211> 383	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> hinge-HCV33-CH2-CH3-SEKDEL	
<400> 57	

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro
 130 135 140

Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160

Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175

Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190

Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205

Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240

Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270

Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285

Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300

Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu
370 375 380

<210> 58

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 58

aggggaccca ggtcaccgtc tcctcagaac c

31

<210> 59

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 59

gagctttgtt gttgaccttg catttgaact ctttccc

37

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 60

caaatgcaag gtcaacaaca aagctc 26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 61

ttcgagctcg aattcttatt atttacccga agactgggtg at 42

<210> 62

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> sequencing primer

<400> 62

ctgaggagac ggtgacctgg gtccct 27

<210> 63

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 63

agcccccgttag ctccctggag ggcctcagt cttcatcttc cccccc 46

<210> 64

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 64

ttcgagctcg aattcttatt atttaccgga agactgggtg atggatttct gggtagtgc 60
g 61

<210> 65

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 65

ttcgagctcg aattcttatt atagctcatc ttacctcgat ttaccgaaactgggtat 60
ggatttctgg gtgttagtgg 79

<210> 66

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (3)..(449)

<400> 66

cc atg gcc cag gtg cag ctg cag gag tct ggg gga ggc ttg gtg cag 47
Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln
1 5 10 15

gct ggg ggg tct ctg agg ctc tcc tgc gca gcc tct gga agc att ttc 95
Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe
20 25 30

aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc
Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg
35 40 45

gag ttg gtc gca ctg att tct gcg ggt ggt cgt aca tgg tat gca gac
Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp
50 55 60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
65 70 75

ctg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat
Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr
80 85 90 95

tac tgt act gcc ggg ggt tcg tac tgg ggc cag ggg acc cag gtc acc
Tyr Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

gtc gcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc gcc cat
Val Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His
115 120 125

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag
His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
130 135 140

gat ctg aat ggg gcc gca tagtaacaat tg
Asp Leu Asn Gly Ala Ala
145

<210> 67

<211> 149

<212> PRT

<213> Artificial Sequence

<220>

<223> VHH with linker

<400> 67

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Arg
20 25 30

Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg Glu
35 40 45

Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
65 70 75 80

